

Supporting Information for

## ***DARC* alleles and Duffy phenotypes in African Americans**

Pirmin Schmid, Kanaeko R. Ravenell, Sherry L. Sheldon, and Willy A. Flegel\*

\* To whom correspondence should be addressed. E-mail: [bill.flegel@nih.gov](mailto:bill.flegel@nih.gov)

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Tables S1 and S2

**Table S1.** DARC genotypes detected in 54 African American blood donors sorted by phenotype and observance

Genotype †		Nucleotide substitution (position) *											Phenotype	Observed (n)	
		5' UTR		Intron (IVS1)					Exon 2			3' UTR			
		-67	+54	+115	+150	-243	-58	125	265	298	+250	+268			
Allele 1	Allele 2	rs2814778	rs863001	rs7550207	rs863002	rs58178708	rs3027016	rs12075	rs34599082	rs13962	rs12042349	rs863003			
<i>FY*B-67C:1</i>	<i>FY*B-67C:1</i>	cc	cc	tt	cc	--	aa	AA	CC	GG	cc	aa	Fy(a-b-)	21	
<i>FY*B-67C:1</i>	<i>FY*B-67C:2</i>	cc	cc	tc	cc	--	aa	AA	CC	GG	cc	aa	Fy(a-b-)	7	
<i>FY*A:1</i>	<i>FY*B-67C:1</i>	tc	cc	tt	cc	t-	aa	GA	CC	GG	cc	aa	Fy(a+b-)	8	
<i>FY*A:1</i>	<i>FY*B-67C:2</i>	tc	cc	tc	cc	t-	aa	GA	CC	GG	cc	aa	Fy(a+b-)	1	
<i>FY*A:2</i>	<i>FY*B-67C:1</i>	tc	cc	tt	cc	--	aa	GA	CC	GG	cc	aa	Fy(a+b-)	1	
<i>FY*A:3</i>	<i>FY*B-67C:1</i>	tc	cc	tt	cc	--	aa	GA	CC	GG	ct	aa	Fy(a+b-)	1	
<i>FY*B:1</i>	<i>FY*B-67C:1</i>	tc	cc	tc	cc	--	ag	AA	CC	GG	cc	aa	Fy(a-b+)	4	
<i>FY*B:2</i>	<i>FY*B-67C:1</i>	tc	cc	tt	ct	--	aa	AA	CC	GG	cc	aa	Fy(a-b+)	3	
<i>FY*B298A:1</i>	<i>FY*B-67C:1</i>	tc	cc	tt	ct	--	aa	AA	CC	GA	cc	ag	Fy(a-b+)	3	
<i>FY*B:3</i>	<i>FY*B-67C:1</i>	tc	cc	tt	cc	--	aa	AA	CC	GG	cc	aa	Fy(a-b+)	2	
<i>FY*B:4</i>	<i>FY*B-67C:1</i>	tc	cc	tt	ct	--	aa	AA	CC	GG	cc	ag	Fy(a-b+)	1	
<i>FY*B298A:1</i>	<i>FY*B-67C:2</i>	tc	cc	tc	ct	--	aa	AA	CC	GA	cc	ag	Fy(a-b+)	1	
<i>FY*B298A:1</i>	<i>FY*X:1</i>	tt	cc	tt	tt	--	aa	AA	CT	AA	cc	gg	Fy(a-b+)	1	
Total														54	

\* Nucleotide substitutions are shown relative to the reference sequence (NG\_011626.1) used for analysis. Nucleotide positions are defined using the first nucleotide of the coding sequence (CDS) of the NM\_002036.2 isoform as nucleotide position 1. Additionally, the rs cluster numbers are shown as found in dbSNP.

† This allele terminology is proposed as an extension of previous nomenclature to be able to reflect the high resolution of the study results (details in Table 3 and text). The allele sequences have been deposited as GenBank accession numbers JN251907 to JN251917.

**Table S2.** Expected and observed Fy phenotype frequencies in African Americans

Phenotype	Expected			Observed	
	Calculation based on alleles *	Frequency	Number †	Number †	Frequency
Fy(a-b-)	$= ({}^{81}/_{108})^2$	56.3 %	30	28	51.9 %
Fy(a+b-)	$= ({}^{11}/_{108})^2 + 2 \times ({}^{11}/_{108}) \times ({}^{81}/_{108})$	16.3 %	9	11	20.4 %
Fy(a-b+)	$= ({}^{16}/_{108})^2 + 2 \times ({}^{16}/_{108}) \times ({}^{81}/_{108})$	24.4 %	13	15	27.7 %
Fy(a+b+)	$= 2 \times ({}^{11}/_{108}) \times ({}^{16}/_{108})$	3.0 %	2	0 ‡	0.0 %
Total		100.0 %	54	54	100.0 %

\* Calculations are made using the data from Table 3.

†  $p = 0.49$ ,  $\chi^2$  test with 2x4 cells, degrees of freedom = 3

‡ The lack of observation of a Fy(a+b+) individual in our study is compatible with the expected number for the size of this study (0 to 3.6 observations; 95% CI, Poisson distribution).